

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:07 ; Search time 88.16 Seconds

(without alignments)
26.590 Million cell updates/sec

Title: US-09-331-631A-37

Perfect score: 52

Sequence: 1 CXXXCXXXXXXXXXXCXXC 20

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	46	4	Q16861
2	52	100.0	47	5	Q9V1Y8
3	52	100.0	48	6	Q9RFP5
4	52	100.0	48	6	P79377
5	52	100.0	48	6	P79380
6	52	100.0	49	5	Q23947
7	52	100.0	49	5	Q23948
8	52	100.0	54	13	Q9Y110
9	52	100.0	57	5	Q9N9H2
10	52	100.0	59	5	P82107
11	52	100.0	59	5	Q9N9H1
12	52	100.0	60	13	Q92044
13	52	100.0	60	13	Q73914
14	52	100.0	60	13	Q93593
15	52	100.0	60	13	Q93609
16	52	100.0	60	13	Q13259
17	52	100.0	60	13	Q13258
18	52	100.0	60	13	Q91B50
19	52	100.0	60	13	Q91910

20	52	100.0	61	6	Q18842	Q18842 balena mys
21	52	100.0	61	6	P79431	P79431 sus scrofa
22	52	100.0	61	6	P79376	P79376 sus scrofa
23	52	100.0	61	6	P79378	P79378 sus scrofa
24	52	100.0	61	6	P79379	P79379 sus scrofa
25	52	100.0	61	6	P79375	P79375 sus scrofa
26	52	100.0	61	6	Q9XST5	Q9XST5 canis faml
27	52	100.0	62	6	Q9T015	Q9T015 canis faml
28	52	100.0	70	13	P82662	P82662 ophiophagus
29	52	100.0	71	5	P76957	P76957 lumbricus t
30	52	100.0	71	10	Q91RED	Q91RED brassica ca
31	52	100.0	71	10	Q91RED	Q91RED brassica ca
32	52	100.0	72	5	Q9V199	Q9V199 drosophila
33	52	100.0	72	6	Q28592	Q28592 ovis aries
34	52	100.0	73	5	Q76953	Q76953 lumbricus c
35	52	100.0	73	5	Q9U569	Q9U569 perna virid
36	52	100.0	73	5	Q9U568	Q9U568 perna virid
37	52	100.0	74	13	Q9Y113	Q9Y113 bungarus mu
38	52	100.0	74	13	Q9Y112	Q9Y112 bungarus mu
39	52	100.0	74	13	Q9Y111	Q9Y111 bungarus mu
40	52	100.0	74	13	Q9Y109	Q9Y109 bungarus mu
41	52	100.0	74	13	Q9Y108	Q9Y108 bungarus mu
42	52	100.0	74	13	Q9Y107	Q9Y107 bungarus mu
43	52	100.0	74	13	Q9Y106	Q9Y106 bungarus mu
44	52	100.0	74	13	Q9Y105	Q9Y105 bungarus mu
45	52	100.0	75	5	Q96858	Q96858 hirudo nipp

ALIGNMENTS

RESULT 1
ID Q16861 PRELIMINARY; PRT; 46 AA.
AC Q16861
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE CYS-TER-1998 (TREMBLrel. 07, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lemasson I., Devaux C., Mesnard J.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U63332; AAB05810.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 46 AA; 5061 MW; 311922FE40A4E8F CRC64;

Query Match 100.0%; Score 52; DB 4; Length 46;
Best Local Similarity 20.0%; Pred. No. 78;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXC 20
Db 11 CCCCCCCCCCCCCCCCCC 30

RESULT 2
ID Q9V1Y8 PRELIMINARY; PRT; 47 AA.
AC Q9V1Y8
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG17567 PROTEIN.
GN CG17567
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Query Match	100.0%	Score 52:	DB 5:	Length 47:
Best Local Similarity	20.0%	Pred. No. 79:		
Matches	4:	Conservative	16:	Mismatches 0; Indels 0; Gaps 0
OY	1	XXXXXXXXXXXXXXXXXXC 20		
DB	2	CCGPGCPRCCDPCGCCYNC 21		
RESULT	3			
Q9RFP5		PRELIMINARY:	PRT:	48 AA.
AC	Q9RFP5			
DT	01-MAY-2000 (TRENBLREL. 13, Created)			
DT	01-MAY-2000 (TRENBLREL. 13, Last sequence update)			
DE	01-MAY-2000 (TRENBLREL. 13, Last annotation update)			
OS	OREZ.			
OC	Mycoplasmata fermentans.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;			
OC	Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=2115;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY;			
RC	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	Seaton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brannon R.C., Rogers Y.-H.C., Blake J.R.G., Champagne M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dudin K.D., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigbam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Li X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,			
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinhart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."			
RL	Science 287:2185-2195(2000).			
DR	EMBL: AE003662; AAF53773.1; -			
DR	FLYBASE: FBgn0040994; CG17567.			
SO	SEQUENCE 47 AA: 4909 MW: 19478A884B86D52 CRC64;			

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RX MEDLINE=99115554; PubMed=9916088
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
RT variation of a major surface lipoprotein and a macrophage-activating
RT lipopeptide of Mycoplasma fermentans.";
RL Infect. Immun. 67:760-771(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PG18;
RA Calcutt M.J., Lavriar J.L., Wise K.S.;
RT "IS1630 of Mycoplasma fermentans, a novel IS30-type insertion element
RT that targets and duplicates inverted repeats of variable length and
RT sequence during insertion.";
RL J. Bacteriol. 181:7597-7607(1999).
DR EMBL; AF179376; AAF1567.1; -.
SQ SEQUENCE 48 AA; 5319 MW; 668836FA3592B2C7 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 48;
Best Local Similarity 20.0%; Pred. No. 80;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0.

QY 1 CXXXCXXXXXXXXXXC 20
|::|::|::|::|::|::|::|
DB 18 CATKCTTKDCCNKCSCC 37

RESULT 4
ID P79377 PRELIMINARY; PRT; 48 AA.
AC P79377;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE METALLOTHIONEIN (MT) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98241500; PubMed=9573337;
RA Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.;
RT "Multiple isoforms of metallothionein are expressed in the porcine
RT liver.";
RL Gene 211:49-55(1998).
CC -I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
CC TRANSCRYPTICALLY REGULATED BY BOTH HEAVY METALS AND
CC GLUCOCORTICOIDS.
CC EMBL; AB000789; BAA19179.1; -.
DR HSSP; P02795; 1MHU.
DR INTERPRO; IPR003019; -.
DR INTERPRO; IPR003019; -.
DR PFAM; PF00131; metalthio, 1.
DR PRINTS; PR00860; MTEVERTEBRATE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
KM Metal-binding: Metal-thiolate cluster; Chelation; zinc.
FT NON_TER 48
FT METAL 24 CLUSTER.
FT METAL 24 CLUSTER.
FT METAL 27 CLUSTER.
FT METAL 17 CLUSTER.
FT METAL 19 CLUSTER.
FT METAL 22 CLUSTER.
FT METAL 31 CLUSTER.
SQ SEQUENCE 48 AA; 4704 MW; F0F5AC96B9EBD19 CRC64;

Query Match 100.0%; Score 52; DB 6; Length 48;
Best Local Similarity 20.0%; Pred. No. 80;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CXXXXXXXXXXXXXXC 20
 ID P79380 PRELIMINARY; PRT; 48 AA.

RESULT 5
 ID P79380 PRELIMINARY; PRT; 48 AA.
 AC P79380;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE METALLOTHIONEIN (MT) (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=98241500; PubMed=9573337;
 RA Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.;
 RT "Multiple isoforms of metallothionein are expressed in the porcine
 liver.";
 RL Gene 211:49-55(1998).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 CC GLUCOCORTICOIDS.
 CC EMBL: AB000795; BAA19184.1; -;
 DR HSSP: P02795; 2MHU.
 DR INTERPRO: IPR000006; -;
 DR PFAM: PF00131; metalthio. 1.
 DR PRINTS: PR00860; MVTERTERATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-chelate cluster; Chelation; Zinc.
 FT NON_TER 48 48
 FT METAL 24 24 CLUSTER.
 FT METAL 27 27 CLUSTER.
 FT METAL 17 17 CLUSTER.
 FT METAL 19 19 CLUSTER.
 FT METAL 22 22 CLUSTER.
 FT METAL 31 31 CLUSTER.
 SQ SEQUENCE 48 AA; 4727 MW; 3BC2E2E8E0686216 CRC64;

Query Match 100.0%; Score 52; DB 6; Length 48;
 Best Local Similarity 20.0%; Pred. No. 80;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXC 20
 ID P79380 PRELIMINARY; PRT; 48 AA.

RESULT 6
 ID Q23947 PRELIMINARY; PRT; 49 AA.
 AC Q23947;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHRC3.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuehn A., Buennemann H.;

RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X58114; CAA41117.1; -;
 DR FLYBASE: FBgn0015096; Dhyd\Mst87fa.
 DR INTERPRO: IPR001450; -;
 DR PROSITE: PS00198; 4FEAS_FERRDOXIN; UNKNOWN.1.
 SQ SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 52; DB 5; Length 49;
 Best Local Similarity 20.0%; Pred. No. 81;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXC 20
 ID Q23948 PRELIMINARY; PRT; 49 AA.

RESULT 7
 ID Q23948 PRELIMINARY; PRT; 49 AA.
 AC Q23948;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHRC2.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuehn A., Buennemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X58114; CAA41118.1; -;
 DR FLYBASE: FBgn0015097; Dhyd\Mst87fb.
 DR INTERPRO: IPR001450; -;
 DR PROSITE: PS00198; 4FEAS_FERRDOXIN; UNKNOWN.1.
 SQ SEQUENCE 49 AA; 4550 MW; 24758FEC51369FID CRC64;

Query Match 100.0%; Score 52; DB 5; Length 49;
 Best Local Similarity 20.0%; Pred. No. 81;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXC 20
 ID Q23948 PRELIMINARY; PRT; 49 AA.

RESULT 8
 ID Q23948 PRELIMINARY; PRT; 49 AA.
 AC Q23948;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
 DE ALPHA-BUNGAROTOXIN ISOFORM R7 (FRAGMENT).
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=8616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RX MEDLINE=99058072; PubMed=9837992;
 RA Liu L.F., Chang C.C., Liao M.Y., Kuo K.W.;
 RT "Genetic characterization of the mRNAs encoding alpha-bungarotoxin:
 RT isoforms and RNA editing in Bungarus multicinctus gland cells.";
 DR EMBL: AF056407; AAC83988.1; -;

DR HSP: P01378; 1ABT.
 DR INTERPRO: IPR000027; -
 DR PFAM: PF00087; toxin; 1.
 FT NON_TER 1
 SQ SEQUENCE 54 AA; 5783 MW; F30BBE6043B62700 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 54;
 Best local Similarity 20.0%; Pred. No. 86;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXCXXC 20
 DB 29 CDAFCSSKGRVGLGCAATC 48

RESULT 9
 Q9N9H2 PRELIMINARY; PRT; 57 AA.
 AC Q9N9H2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes philippinarum.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
 OC Veneroidae; Veneridae; Ruditapes.
 OX NCBI_TaxID=104384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL.
 RA Moraga D., Tanguy A.;
 RT "Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 RT pullastra";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249686; CAB96403.1; -
 FT NON_TER 1
 FT NON_TER 57
 SQ SEQUENCE 57 AA; 5411 MW; F7B37567623FD7DD CRC64;

Query Match 100.0%; Score 52; DB 5; Length 57;
 Best local Similarity 20.0%; Pred. No. 88;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXCXXC 20
 DB 23 CGPGCKGDCGCKGCKVC 42

RESULT 10
 P82107 PRELIMINARY; PRT; 59 AA.
 AC P82107;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE BDELLASTASIN (BDELLIN A).
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Atychobdellida; Hirudiniiformes; Hirudinae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RA Moser M., Auerswald E., Mentele R., Eberskorn C., Fritz H., Fink E.;
 RT "Bdelastatin, a serine protease inhibitor of the antistatin family
 RT from the medical leech (Hirudo medicinalis). Primary structure,
 RT expression in yeast, and characterization of native and recombinant
 RT inhibitor";
 RL Eur. J. Biochem. 253:212-220(1998).
 CC -I- FUNCTION: STRONG INHIBITOR OF MAMMALIAN TRYPSIN, PLASMIN AND

CC ACROSIN.
 CC -I- MASS SPECTROMETRY: MW=6332.6; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE ANTISTATIN FAMILY.
 DR HSP: P80302; 1HIA.
 KW Serine protease inhibitor.
 FT ACT_SITE 34 35
 FT DISULFID 10 21
 FT DISULFID 15 26
 FT DISULFID 28 48
 FT DISULFID 33 52
 FT DISULFID 37 54
 SQ SEQUENCE 59 AA; 6343 MW; 43BA5BB2D0E403A9 CRC64;

Query Match 100.0%; Score 52; DB 5; Length 59;
 Best local Similarity 20.0%; Pred. No. 90;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXCXXC 20
 DB 33 CKVCEHGFKKDNCEYAC 52

RESULT 11
 Q9N9H1 PRELIMINARY; PRT; 59 AA.
 AC Q9N9H1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes decussatus.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
 OC Veneroidae; Veneridae; Ruditapes.
 OX NCBI_TaxID=104385;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D., Tanguy A.;
 RT "Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 RT pullastra";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249687; CAB96402.1; -
 FT NON_TER 1
 FT NON_TER 59
 SQ SEQUENCE 59 AA; 5613 MW; CAB87C9FE35EC8A2 CRC64;

Query Match 100.0%; Score 52; DB 5; Length 59;
 Best local Similarity 20.0%; Pred. No. 90;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXCXXC 20
 DB 10 CVSCSDSCPAFGCKGPGC 29

RESULT 12
 Q92044 PRELIMINARY; PRT; 60 AA.
 AC Q92044;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE METALLOTHIONEIN (MT).
 GN MT A.
 OS Cyprinodon sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphi; Atherinomorpha;
 OC Cyprinodontiformes; Cyprinodontidae; Cyprinodon.

OX NCBI_TaxId=48417;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Kille P., Olsson P.E.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: X97273; CA65928.1; -
DR HSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -
DR PFAM: PF00131; metalthio.1.
DR PRINTS: PR00860; MVERTBERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc.
FT METAL 14 14 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.
FT METAL 20 20 CLUSTER.
FT METAL 21 21 CLUSTER.
FT METAL 22 23 CLUSTER.
FT METAL 23 25 CLUSTER.
FT METAL 25 25 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 28 28 CLUSTER.
FT METAL 30 30 CLUSTER.
SQ SEQUENCE 60 AA; 6095 MW; F73A5EE39CDBD971 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXCXXC 20
|:::|:::|:::|:::|:::|:::|
DB 28 CKRSCCPCSGCTKCAAGC 47

RESULT 13
073914
ID 073914 PRELIMINARY; PRT; 60 AA.
AC 073914;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod),
and Chionodactylus rastrospinosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Nototheniidae; Notothenia.
OX NCBI_TaxId=8209, 34790;
RN [1]
RP SEQUENCE FROM N.A.
RA Scudiero R., Verde C., Cargnale V., Capasso C., di Prisco G.,
Parisi E.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cargnale V., Capasso C., Scudiero R., Parisi E.;
RT "Metallothionein in Antarctic organisms";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: AJ006484; CA07063.1; -
DR EMBL: AJ011584; CA09714.1; -;

DR HSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -
DR INTERPRO: IPR003019; -
DR PFAM: PF00131; metalthio.1.
DR PRINTS: PR00860; MVERTBERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc.
FT METAL 23 23 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.
FT METAL 21 21 CLUSTER.
FT METAL 30 30 CLUSTER.
SQ SEQUENCE 60 AA; 6019 MW; E86E7155A2C424A CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXCXXC 20
|:::|:::|:::|:::|:::|:::|
DB 28 CKRSCCPCSGCTKCAAGC 47

RESULT 14
093593
ID 093593 PRELIMINARY; PRT; 60 AA.
AC 093593;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT.
OS Chaenocephalus aceratus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Channichthyidae; Chaenocephalus.
OX NCBI_TaxId=36190;
RN [1]
RP SEQUENCE FROM N.A.
RA Cargnale V., Capasso C., Scudiero R., Parisi E.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
GLUCOCORTICOIDS.
CC EMBL: AJ011583; CA09713.1; -
DR HSP: P02802; 1DFS.
DR INTERPRO: IPR000006; -
DR INTERPRO: IPR003019; -
DR PFAM: PF00131; metalthio.1.
DR PRINTS: PR00860; MVERTBERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc.
FT METAL 23 23 CLUSTER.
FT METAL 26 26 CLUSTER.
FT METAL 16 16 CLUSTER.
FT METAL 18 18 CLUSTER.
FT METAL 21 21 CLUSTER.
FT METAL 30 30 CLUSTER.
SQ SEQUENCE 60 AA; 6017 MW; E8773344264C424A CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXCXXC 20
|:::|:::|:::|:::|:::|:::|

